

T n2274

1381 ATGTTCCAAAACAAATGACATGCTATATTTCGAGAGTATCACGTGGATCGAGTGATCAAAA 1440
 V P K Q M T C Y I R E Y H V D R V I K K
 130 140

Intron 1

1441 AGCTCGACGAGATGTGTGATTTAGGTGAGAAACTGGAAGCTCTCGTGTATTATTATAATC
 L D E M C D L D
 150

1501 TTGCTTAAACTTCAGACTCCTTTTTTCTGTTTCTACACGGCCGAGCTGGATCCGGAAAAAT 1560
 S F F L F L R G R A G S G . K S
 160

Intron 2

1561 CAGTAATTGCATCACAAGCTCTTTTCGAAATCTGACCAACTTATTGGAATGTGAGTGGTAT 1620
 V I A S Q A L S K S D Q L I G I
 170 180

1621 TATCTGAATCTACGGATCTTCATTCTATTACAGAAATTATGATTCAATCGTTTGGCTCAA 1680
 N Y D S I V W L K
 190

1681 AGATAGTGGAAACAGCTCCAAAATCTACATTGATTATTTACGGATATTTGCTGATGCT 1740
 D S G T A P K S T F D L F T D I L L M L
 200 210

A n1920/n2247
 Intron 3

1741 AAAGTGAGTGAATAGAGTGCATGTAACATTCAGCATGATTTTGAAATTATGAAAATTGA 1800
 K
 CCTGGTTAGCTTTTAATTTCATATTTTCGTGACGCTTGCATGTTTGTGTGTTGAAGACG
 1801 1860
 AGCCCGTGTTGTGAGCGACACGGATGACTCGCATTTCGATCACCAGCTTCATTAAACCGTGT
 1861 1920

A n2273

1921 TCTTTCAAGCAGCGAAGACGATCTTCTCAATTTCCCATCGGTGGAGCATGTCACGTCAGT 1980
 S E D D L L N F P S V E R V T S V
 220

Intron 4

1981 TGTACTCAAAAGGATGCTAAGTTGCTTGCCGATTCTGGTACAATATCTTAAATTATTGGT 2040
 V L K R M
 230

2041 TTTTACATCTGCAACGCACCTCATTGATCGTCCAAATACTTTATTCGTATTTGATGACGTA 2100
 I C N A L I D R P N T L F V F D D V
 240 250

A n1948 T n1947

2101 GTTCAAGAAGAAACAATTTCGTTGGGCTCAGGAGCTACGTCTTCGATGTCTTGTAACACTACT 2160
 V Q E E T I R W A Q E L R L R C L V T T
 260 270

2161 CGTGACGTGGAAATATCAAAATGCTGCTTCTCAAACATGCGAATTCATTGAAGTGACATCA 2220
 R D V E I S N A A S Q T C E F I E V T S
 280 290

FIGURE 1

TTGAAATCGATGAATGTTATGATTTTCTAGAAGCTTATGGAATGCCGATGCCTGTTGGA
 2221 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2280
 L E I D E C Y D F L E A Y G M P M P V G
 300 310
 Tc4 n1416
 GAAAAAGAAGAAGATGTGCTTAATAAAACAATCGAACTAAGCAGTGGAAATCCAGCAACG
 2281 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2340
 E K E E D V L N K T I E L S S G N P A T
 320 330
 CITATGATGTTTTTCAAGTCTTGTGAACCGAAAACATTTGAAAAGTGAGTGGGACATACC
 2341 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2400
 L M M F F K S C E P K T F E K
 330
 AATTTGAGACTTTTAAATAATTTATTCTACAATAAAAGTTAATCAAAAAGTTTCATAGC
 2401 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2460
 TGATTGTCTTTAAATTTTACGAATTGAGGATCAAAATCAAGAATTAGGATCCTGGCAGCA
 2461 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2520
 GAGAAAAGTGTGTAGCTACCGTACCGAGAGATTCTTGATATTGCCATCGATTTAAT
 2521 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2580
 TTTTAAAGAAATTATCGTTTTACATAATTGAACAAGAGATACACGGTCTCGACCCGACG
 2581 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2640
 GAAATTTTTTAAATGAAAGCGAGTATGAGCCTGTTTCATTATTTTCGATTTTCTCTTG
 2641 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2700
 TTGTTCTTTTTATTTAAAGCCTTTTATTTTGAACAAGTCTAAAAATATTAAAACTGA
 2701 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2760
 ATAAAAATTTTAAAAAAATCAAGTAAAATAGAAAAACAGCAAGGCTGGAGACTACTGTA
 2761 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2820
 CTTCTTAAATCCGCATACTCTTTTTATTTAATCATTTTCCGGAATGTCGAAACGAAATAA
 2821 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2880
 TACATTTTATGTCGAAATCGCTAGGTATATTCTTAAATATCAAAACATTTTGCATTCA
 2881 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2940
 GATGGCACAGCTTAATAACAAATTGAAAGTCGAGGATTAGTCGGTGTGAATGTATCA
 2941 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 3000
 M A Q L N N K L E S R G L V G V E C I T
 340 350
 CCCCTTACTCGTACAAGTCACTCGCAATGGCTCTTCAAAGATGTGTTGAAGTTTTGTCAG
 3001 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 3060
 P Y S Y K S L A M A L Q R C V E V L S D
 360 370
 ATGAGGATCGAAGTGCTCTTGCTTTCCGAGTTGTGATGCCTCCTGGAGTTGATATACCCG
 3061 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 3120
 E D R S A L A F A V V M P P G V D I P V
 380 390
 A n1894
 TCAAGCTATGGTCATGTGTTATTCCAGTTGATATTGTTCAAATGAAGAAGAACAATTGG
 3121 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 3180
 K L W S C V I P V D I C S N E E E Q L D
 400 410
 ATGATGAAGTTGCGGATCGGTTGAAAAGACTCAGCAGTATGAGTCTTGAAATTTGAAGA
 3181 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 3240
 D E V A D R L K R L S K
 420
 TTTAAATTAACACTTAAATTTTCAAGCGTGGAGCTCTTCTCAGTGGAAAACGAATGCCCG
 3241 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 3300
 R G A L L S G K R M P V
 430 440

FIGURE 1

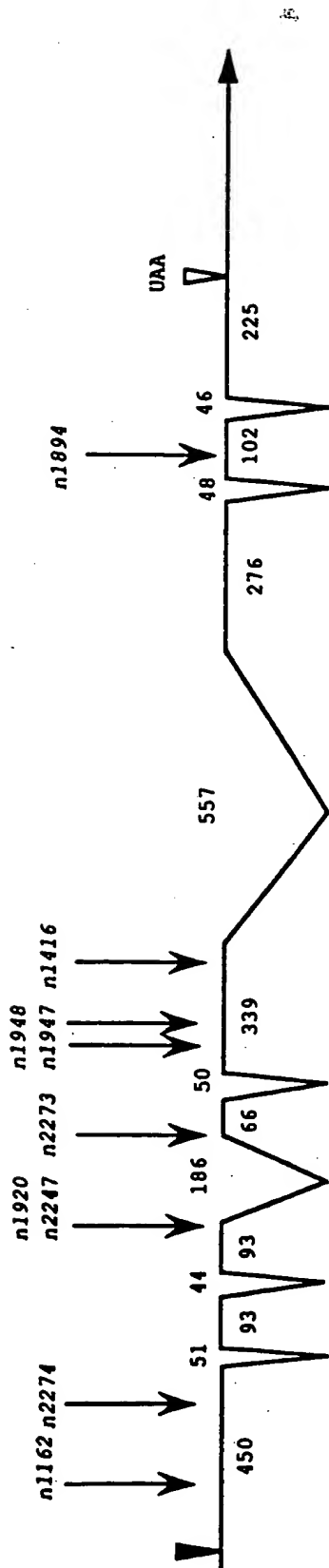


FIGURE 2

	10	12	14	18	21
	X	Y	Z	-X	-Z
	D	N	S	T	E
Calcium-binding loop consensus		D	N	S	
			D	E	
				Q	
				D	
				N	
EF-hand consensus	O	*	O	*	O
	G	*	*	O	*
					E
ced-4 sequence 1	Y	N	N	Q	S
	H	L	A	D	F
	L	E			
sequence 2	S	L	E	I	D
	E	C	Y	D	F
	L	E			
Parvalbumin (carp)	D	Q	D	K	S
(hake)	D	Q	D	K	D
(ray)	D	S	D	G	D
	H	K	I	G	V
	D	E	D	E	E
SCBP (<i>Amphioxus</i> I)	D	I	N	K	D
	D	V	V	S	W
	E	E	E	E	E
ICaBP (bovine)	A	K	E	G	D
	D	K	N	G	D
	P	Q	L	S	K
	E	V	S	F	E
	E	E	E	E	E
Troponin C (rabbit)	D	A	D	G	G
	D	E	D	G	S
	D	R	N	A	D
	D	K	N	N	D
	G	Y	I	D	A
	G	R	I	D	F
	D	E	E	E	E
Calmodulin (bovine)	D	K	D	G	N
	G	T	I	T	T
	K	E	E	E	E
Trypsinogen	L	G	E	D	N
	I	N	V	V	E
	G	N	E	E	E
Fibrinogen	D	N	D	N	D
	K	F	E	G	N
	C	A	E	E	E
Villin	G	V	D	P	S
	R	K	E	N	H
	L	S	E	E	E
GBP	D	L	N	K	D
	G	Q	I	Q	I
	E	E	E	E	E

FIGURE 3

[illegible]

FIGURE 4

[illegible]

FIGURE 4

2581 TTTTAAAGTTTCGGCGCAAAAGCAAGGGTCTCACGGAAAAAGAGGCGGATCGTAATTTT 2640
 -----+-----+-----+-----+-----+
 2641 GCAACCCACCGGCACGGTTTTTCTCCTCCGAAATCGGAAATTATGCACTTTCCCAAATAT 2700
 -----+-----+-----+-----+-----+
 2701 TTGAAGTGAAATATATTTTACTGAAAGCTCGAGTGATTATTTATTTTAACTA 2760
 -----+-----+-----+-----+-----+
 2761 ATTTTCGTGGCGCAAAAGGCCATTTGTAGATTGCGGAAATACTTGTACACACACAC 2820
 -----+-----+-----+-----+-----+

 2821 ACACACATCTCCTTCAAATATCCCTTTTTCCAGTGTGACTCGAATGCTGTGAATTCTGA 2880
 -----+-----+-----+-----+-----+
 V D S N A V E F E
 100

 2881 GTGTCCAATGTCACCGGCAAGCCATCGTCCGAGCCGCGCATTGAGCCCCGCGGCTACAC 2940
 -----+-----+-----+-----+-----+
 C P M S P A S H R R S R A L S P A G Y T
 110 120

 2941 TTCACCGACCCGAGTTACCGTGACAGCGTCTCTTCAGTGTCACTTCATTCTTATCA 3000
 -----+-----+-----+-----+-----+
 S P T R V H R D S V S S V S S F T S Y Q
 130 140

 3001 GGATATCTACTCAAGAGCAAGATCTCGTTCTCGATCGCGTGCATTTCATTTCATCGGATCG 3060
 -----+-----+-----+-----+-----+
 D I Y S R A R S R S R S R A L H S S D R
 150 160

 3061 ACACAATTATTCATCTCCTCCAGTCAACGCATTTCCAGCCAACCTTGTATGTTGATGCG 3120
 -----+-----+-----+-----+-----+
 H N Y S S P P V N A F P S Q P S
 170

 Repeat 1

 3121 AACACTAAATTCTGAGAATGCGCATTACTCAACATATTTGACGCGCAAATATCTCGTAGC 3180
 -----+-----+-----+-----+-----+

 3181 GAAAAATACAGTAACCCTTTAAATGACTATTGTAGTGTGATTACGGGCTCGATTTTCG 3240
 -----+-----+-----+-----+-----+

 -->
 3241 AAACGAATATATGCTCGAATTGTGACAACGAATTTTAATTTGTCATTTTGTGTTTTCTT 3300
 -----+-----+-----+-----+-----+

 Repeat 1

 3301 TTGATATTTTGTATCAATTAATAAATTATTTCCGTAAACAGACACCAGCGCTACAGTACT 3360
 -----+-----+-----+-----+-----+

 3361 CTTTAAAGAGTTACAGTAGTTTTCGCTTCAAGATATTTGAAAAGAATTTTAAACATTT 3420
 -----+-----+-----+-----+-----+

 3421 TGAAAAAAATCATCTAACATGTGCCAAAACGCTTTTTTCAAGTTTCGCAGATTTTGTGA 3480
 -----+-----+-----+-----+-----+

FIGURE 4

3481	TTTTTTCATTCAAGATATGCTTATTAACACATATAATTATCATTAATGTGAATTTCTTG -----+-----+-----+-----+-----+-----+-----+	3540
3541	TAGAAATTTTGGGCTTTTCGTTCTAGTATGCTCTACTTTTGAAATTGCTCAACGAAAAA -----+-----+-----+-----+-----+-----+-----+	3600
3601	TCATGTGGTTTGTTTCATATGAATGACGAAAAATAGCAATTTTTTATATATTTCCCTAT -----+-----+-----+-----+-----+-----+-----+	3660
3661	TCATGTGTGCAGAAAAATAGTAAAAAGCGCATGCATTTTTTCGACATTTTTTACATCGA -----+-----+-----+-----+-----+-----+-----+	3720
3721	ACGACAGCTCACTTCACATGCTGAAGACGAGAGACGCGGAGAAATACCACACATCTTCT -----+-----+-----+-----+-----+-----+-----+	3780
3781	Repeat 2 GCGTCTCTCGTCTTCAGCATGTGAAATGGGATCTCGGTGCATGTAAAAAATGTCGAATA -----+-----+-----+-----+-----+-----+-----+	3840
3841	ATGTAAAAAATGCATGCGTTTTTTTTACACTTTTCTGCACAAATGAATAGGGGGAAAAATGT -----+-----+-----+-----+-----+-----+-----+	3900
3901	ATTAAAAATACATTTTTTTGTATTTTTCAACATCACATGATTAACCCCATTTTTCGTT -----+-----+-----+-----+-----+-----+-----+	3960
3961	GAGCAACTTAAAAAGTAGAGAATATTAGAGCGAAAAACCAAATTTCTTCAAGATATTACC -----+-----+-----+-----+-----+-----+-----+	4020
4021	TTTATTGATAATTATAGATGTTAATAAGCATATCTTGAATGAAAGTCAGCAAAAATATGT -----+-----+-----+-----+-----+-----+-----+	4080
4081	GCGAAACACCTGAAAAAATCAAAAATTCTGCGAAAATTGAAAAATGCATTAAATACA -----+-----+-----+-----+-----+-----+-----+	4140
4141	TTTTTGCATTTTTCTACATCACATGAATGTAGAAAATTAAAGGGAAATCAAAATTTCTA -----+-----+-----+-----+-----+-----+-----+	4200
4201	GAGGATATAATTGAATGAAACATTGCGAAATTAAATGTGCGAAACGTCAAAAAAGAGGA -----+-----+-----+-----+-----+-----+-----+	4260
4261	AATTTGGGTATCAAAATCGATCCTAAAACCAACACATTTTCAGCATCCGCCAACTCTTCAT -----+-----+-----+-----+-----+-----+-----+	4320

S A N S S F
180

FIGURE 4

4321 TCACCGGATGCTCTTCTCTCGGATACAGTTCAAGTCGTAATCGCTCATTGAGCAAAGCTT 4380
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 T G C S S L G Y S S S R N R S F S K A S
 190 200
 4381 CTGGACCAACTCAATACATATTCCATGAAGAGGATATGAACTTTGTCGATGCACCAACCA 4440
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 G P T Q Y I F H E E D M N F V D A P T I
 210 220
 4441 TAAGCCGTGTTTTTCGACGAGAAAACCATGTACAGAACTTCTCGAGTCCTCGTGAATGT 4500
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 S R V F D E K T M Y R N F S S P R G M C
 230 240
 4501 GCCTCATCATAAATAATGAACACTTTGAGCAGATGCCAACACGGAATGGTACCAAGGCCG 4560
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 L I I N N E H F E Q M P T R N G T K A D
 250 260
 4561 ACAAGGACAATCTTACCAATTTGTTTCAGATGCATGGGCTATACGGTTATTTGCAAGGACA 4620
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 K D N L T N L F R C M G Y T V I C K D N
 270 280
 | intron 4
 4621 ATCTGACGGGAAGGGTACGGCGAAATTATATTACCCAAACGCGAAATTTGCCATTTTGGC 4680
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 L T G R
 Repeat 3
 ----->
 4681 CCGAAAATGTGGCGCCCGTCTCGACACGACAATTTGTGTTAAATGCAAAAATGTATAAT 4740
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 4741 TTTGCAAAAACAAAATTTTGAACTTCCGCGAAAATGATTTACCTAGTTTCGAAATTTTC 4800
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 4801 GTTTTTTCCGGCTACATTATGTGTTTTTCTTAGTTTTTCTATAATATTTGATGTAAAAA 4860
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 4861 ACCGTTTGTAATTTTCAGACAATTTTCCGCATACAAAACCTTGATAGCAGGAAATCAATT 4920
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 4921 TTCTGAATTTTCAAAATTATCCAAAATGCACAATTTAAAATTTGTGAAAATTGGCAAAC 4980
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 4981 GGTGTTTCAATATGAAATGTATTTTTTAAAACTTTAAAAACCACTCCGAAAAGCAATAA 5040
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 5041 AAATCAAAACAACGTCACAATTCAAATTCAAAAGTTATTCATCCGATTGTTTATTTTGG 5100
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 5101 CAAAATTTGAAAAATCATGAAGGATTTAGAAAAGTTTTATAACATTTTCTAGATTTT 5160
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 5161 TCAAAATTTTTTTTAAACAAATCGAGAAAAAGAGAATGAAAATCGATTTTAAAAATATCC 5220
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 Repeat 3
 <-----
 5221 ACAGCTTCGAGAGTTTGAAATTACAGTACTCCTTAAAGGCGCACACCCCATTTGCATTGG 5280
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

 5281 ACCAAAAATTTGTCGTGTCGAGACCAGGTACCGTAGTTTTTGTGCAAAAATTGCACCAT 5340
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 5341 TGGACAATAAACCTTCCTAATCACCAAAAAGTAAAATTGAAATCTTCGAAAAGCCAAAAA 5400
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

FIGURE 4

5401 ATTCAAAAAAAAAAGTCGAATTTTCGATTTTTTTTTTGGTTTTTTGGTCCCAAAAACCAAAA 5460
 -----+-----+-----+-----+-----+-----+-----+-----+-----+
 5461 AAATCAATTTTCTGCAAAATACCAAAAAGAAACCCGAAAAAATTTCCAGCCTTGTTCCT 5520
 -----+-----+-----+-----+-----+-----+-----+-----+-----+
 5521 AATGTAAACTGATATTTAATTTCCAGGGAATGCTCCTGACAATTCGAGACTTTGCCAAAC 5580
 -----+-----+-----+-----+-----+-----+-----+-----+-----+
 G M L L T I R D F A K H
 290 300
 5581 ACGAATCACACGGAGATTCTGCGATACTCGTGATTCTATCACACGGAGAAGAGAATGTGA 5640
 -----+-----+-----+-----+-----+-----+-----+-----+-----+
 E S H G D S A I L V I L S H G E E N V I
 310 320
 5641 TTATTGGAGTTGATGATATACCGATTAGTACACACGAGATATATGATCTTCTCAACGCGG 5700
 -----+-----+-----+-----+-----+-----+-----+-----+-----+
 I G V D D I P I S T H E I Y D L L N A A
 330 340
 A(n2433)
 5701 CAAATGCTCCCGTCTGGCGAATAAGCCGAAAATCGTTTTTGTGCAGGCTTGTTCGAGGCG 5760
 -----+-----+-----+-----+-----+-----+-----+-----+-----+
 N A P R L A N K P K I V F V Q A C R G E
 350 360
 intron 5
 5761 GTTCGTTTTTTATTTTAATTTTAATATAAAATATTTTAAATAAAATTCATTTTCAGAACGTC 5820
 -----+-----+-----+-----+-----+-----+-----+-----+-----+
 R R
 5821 GTGACAATGGATTCCCGAGTCTTGGATTCTGTGACGGAGTTCCTGCATTTCTTCGTCGTG 5880
 -----+-----+-----+-----+-----+-----+-----+-----+-----+
 D N G F P V L D S V D G V P A F L R R G
 370 380
 T(n1165)
 5881 GATGGGACAATCGAGACGGGCCATTGTTCAATTTTCTTGGATGTGTGCGGCCGCAAGTTC 5940
 -----+-----+-----+-----+-----+-----+-----+-----+-----+
 W D N R D G P L F N F L G C V R P Q V Q
 390 400
 intron 6
 5941 AGGTTGCAATTTAATTTCTTGAATGAGAATATTCCTTCAAAAAATCTAAAATAGATTTTT 6000
 -----+-----+-----+-----+-----+-----+-----+-----+-----+
 6001 ATTCCAGAAAGTCCCGATCGAAAAATTGCGATATAATTACGAAATTTGTGATAAAATGAC 6060
 -----+-----+-----+-----+-----+-----+-----+-----+-----+
 Repeat 4
 6061 AAACCAATCAGCATCGTCGATCTCCGCCCACTTCATCGGATTGGTTTGAAAGTGGGCGGA 6120
 -----+-----+-----+-----+-----+-----+-----+-----+-----+
 ----->
 6121 GTGAATTGCTGATTGGTCGCAGTTTTTCAGTTTAGAGGGAATTTAAAAATCGCCTTTTCGA 6180
 -----+-----+-----+-----+-----+-----+-----+-----+-----+
 6181 AAATTAATAATGATTTTTTCAATTTTTTCGAAAAATATTCGATTATTTTATATTCTTT 6240
 -----+-----+-----+-----+-----+-----+-----+-----+-----+

FIGURE 4

A(n717)
|

6241 GGAGCGAAAGCCCCGTCCTGTAAACATTTTAAATGATAATTAATAAATTTTGCAGCAA 6300
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
Q

T(n1949)
|

6301 GTGTGGAGAAAGAAGCCGAGCCAAGCTGACATTCTGATTGCGATACGCAACGACAGCTCAA 6360
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
V W R K K P S Q A D I L I R Y A T T A Q
410 420

A(n1286)
|

6361 TATGTTTCGTGGAGAAACAGTGCTCGTGGATCATGGTTCATTCAAGCCGTCTGTGAAGTG 6420
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
Y V S W R N S A R G S W F I Q A V C E V
430 440

T(n1129,n1164)
|

6421 TTCTCGACACACGCAAAGGATATGGATGTTGTTGAGCTGCTGACTGAAGTCAATAAGAAG 6480
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
F S T H A K D M D V V E L L T E V N K K
450 460

T(n2430) | A(n2426) | | intron 7

6481 GTCGCTTGTGGATTTTCAGACATCACAGGGATCGAATATTTTGAAACAGATGCCAGAGGTA 6540
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
V A C G F Q T S Q G S N I L K Q M P E
470 480

Repeat 5

6541 CTTGAAACAAACAATGCATGTCTAACTTTTAAGGACACAGAAAAATAGGCAGAGGCTCCT 6600
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
----->

6601 TTTGCAAGCCTGCCGCGCTCAACCTAGAATTTTAGTTTTAGCTAAATGATTGATTTT 6660
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
6661 GAATATTTTATGCTAATTTTGTGCTTAAATTTTGAAATAGTCACTATTTATCGGGTTT 6720
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
6721 CCAGTAAAAAATGTTTATTAGCCATTGGATTTTACTGAAAACGAAAATTTGTAGTTTTTC 6780
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
6781 AACGAAATTTATCGATTTTAAATGTAAAAAATAGCGAAATTACATCAACCATCAA 6840
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
6841 GCATTTAAGCCAAAATTGTAACTCATTAAAAATTAATTCAAAGTTGTCCACGAGTATT 6900
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
-----<

Repeat 5

6901 ACACGGTTGGCGCGCGCAAGTTTGCAAAACGACGCTCCGCCTCTTTTCTGTGCGGCTT 6960
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

T(n1163)
|

6961 GAAAACAAGGGATCGGTTTAGATTTTCCCAAAATTTAAATTAAATTTTCAGATGACATC 7020
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
M T S

FIGURE 4

7021 CCGCCTGCTCAAAAAGTTCTACTTTTGGCCGGAAGCACGAAACTCTGCCGTCTAAAATTC 7080
 -----+-----+-----+-----+-----+-----+-----+
 R L L K K F Y F W P E A R N S A V *
 490 500
 7081 ACTCGTGATTCAATTGCCCAATTGATAATTGTCTGTATCTTCTCCCCCAGTTCTCTTTTCGC 7140
 -----+-----+-----+-----+-----+-----+-----+
 CCAATTAGTTTAAACCATGTGTATATTGTTATCCTATACTCATTTCACTTTATCATTCT 7141
 -----+-----+-----+-----+-----+-----+-----+
 ATCATTCTCTTCCCATTTCACACATTTCATTCTCTACGATAATCTAAAATTATGAC 7200
 -----+-----+-----+-----+-----+-----+-----+
 7201 GTTTGTGTCTCGAACGCATAATAATTTTAATAACTCGTTTGAATTTGATTAGTTGTTGT 7260
 -----+-----+-----+-----+-----+-----+-----+
 7261 GCCCAGTATATATGTATGTACTATGCTTCTATCAACAAAATAGTTTCATAGATCATCACC 7320
 -----+-----+-----+-----+-----+-----+-----+
 7321 CCAACCCACCAACCTACCGTACCATATTTCATTTTGGCCGGAATCAATTCGATTAATT 7380
 -----+-----+-----+-----+-----+-----+-----+
 7381 TTAACCTATTTTTTCGCCACAAAAATCTAATATTTGAATTAACGAATAGCATTCCCATC 7440
 -----+-----+-----+-----+-----+-----+-----+
 7441 TCTCCCGTGCCGGAATGCCTCCCGGCCTTTTAAAGTTCGGAACATTTGGCAATTATGTAT 7500
 -----+-----+-----+-----+-----+-----+-----+
 7501 AAATTTGTAGGTCCCCCCCATCATTTCCCGCCCATCATCTCAAATTGCATTCTTTTTTCG 7560
 -----+-----+-----+-----+-----+-----+-----+
 7561 CCGTGATATCCCGATTCTGGTCAGCAAAGATCT 7620
 -----+-----+-----+-----+-----+-----+-----+
 7621 -----+-----+-----+-----+-----+-----+-----+ 7653

FIGURE 4

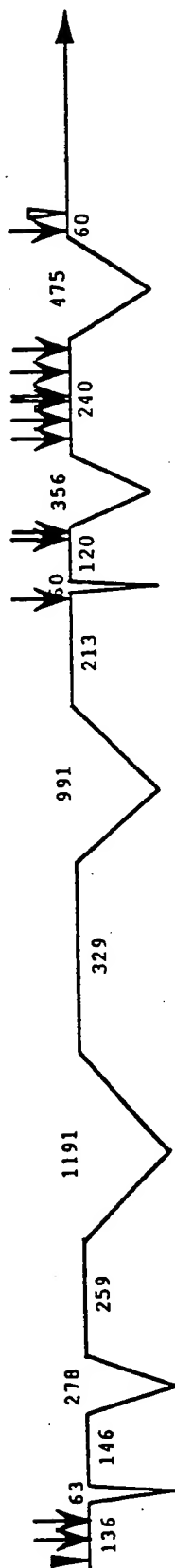


FIGURE 5A

ced-3 Mutations are Clustered

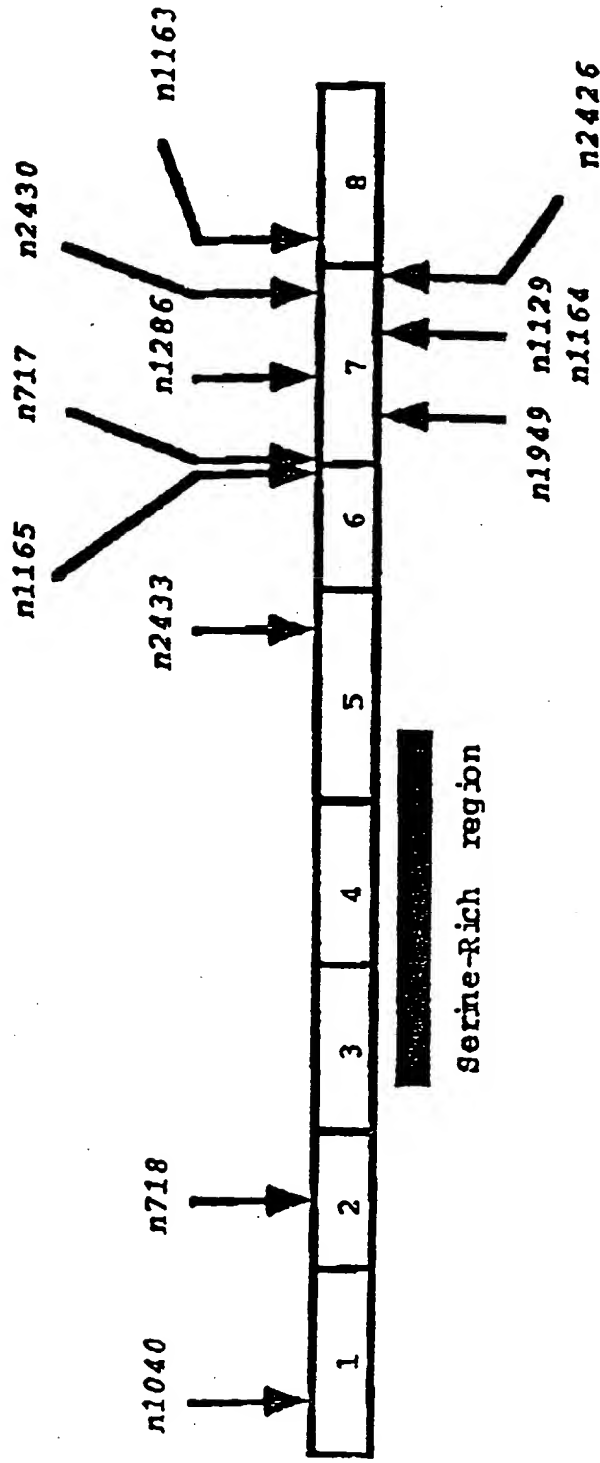


FIGURE 5B

06E02T-B2F7B680

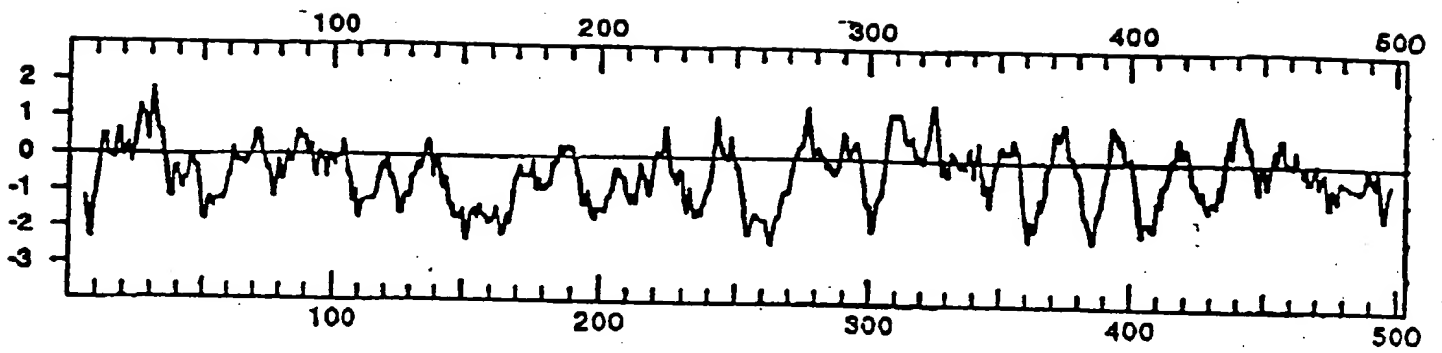


FIGURE 6

1	01	MMRQDRRSLLERNIMMFSSHLKVDEILEVLIAKQVLNSDNGDMINSCGTV	50
2	W.....LE...K.QA.L..D.....V....R.E	
3		TVS\SLI..R.....M.....	
1	51	REKRREIVKAVQRPQDVAFDAFYDALRSTGHEGLAEVLEPLARSVDSNAV	100
2		.DNEK.....R..E.....D...ND..D..M..S.P..P.	
3			
1	101	EFECPMSPASHRRSRALSPAGYTSPTVRHRDSVSSVSSTFS_YQDIYSRA	149
2		PM.....S.....P..A.....I.....T...V....	
3			S
1	150	RSRSR_SRALHSSDRHNYSSPPVNAFSPQSSANSSTGCSLGYSSSRN	198
2		..S...S...P.Q.....M.AA_TS.....A.....	
3		T...__..P..T.....V..S...S.Q...A.....S.....T	
1	199	RSFSKASGPTQYIFHEEDMNFVDAPTISRVFDEKTMYNFSSPRGMCLI	247
2	T.AQS.....Y.....H.....L...	
3		..Y....AHS.....Y.....H.....T...L...	
1	248	INNEHFQMPTRNGTKADKDNLTNLFRCMGYTVICKDNLTGRGMLLTIRD	297
2	I.....E..S...S	
3	P....IS.....I.H.....M.....	
1	298	FAKHESHGDSAILVILSHGEENVIIGVDDIPISTHEIYDLLNAANAPRLA	347
2		.GRNDM.....VSVNV.....	
3		...N.T.....VSVNV....X.....	
1	348	NKPKIVFVQACRGERRDNGFPVLDSVDGVP AFLRRGWDNRDGPLFNFLGC	397
2	L.....SLI.....	
3	L.....V.....LI.....KG.....	
1	398	VRPQVQQVWRKKPSQADILIRYATTAQYVSWRNSARGSWFIQAVCEVFST	447
2	M..A.....L	
3	A.....A.....L	
1	448	HAKDMDVVELLTEVNKKVACGFQTSQGSNILKQMPMTSRLKKFYFWPE	497
2	L.....	
3	A.....L.....	
1	498	ARN SAV 503	
2		DRG.....	
3		D..RS...	

FIGURE 7

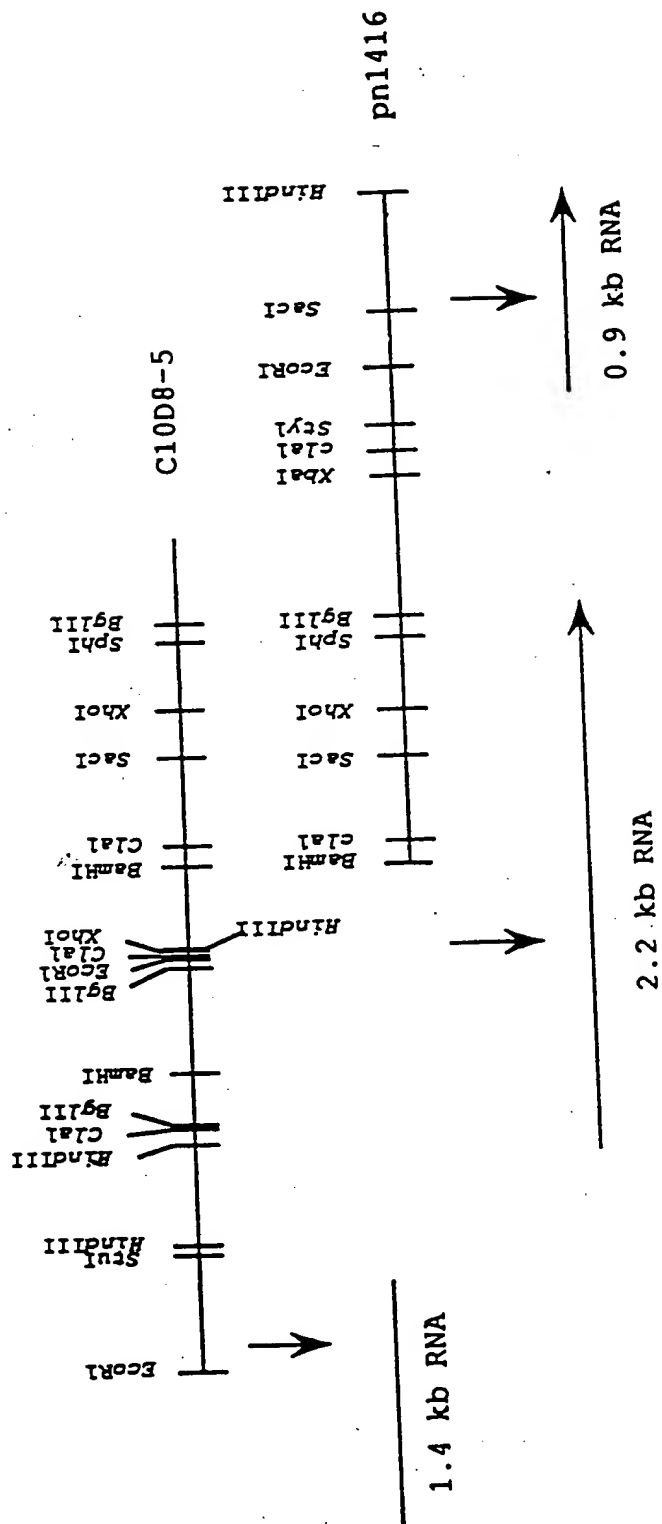


FIGURE 8

IV

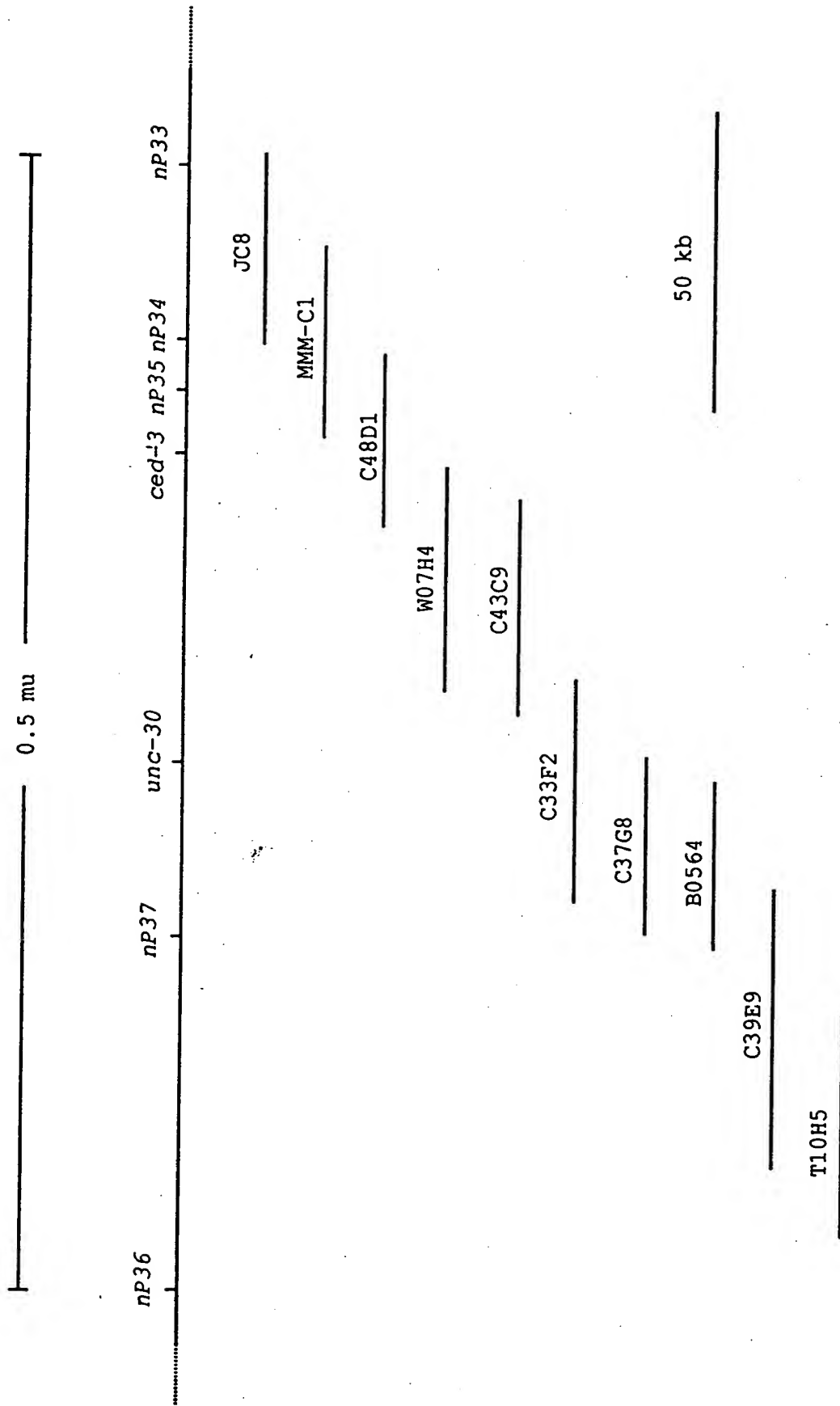


FIGURE 9

